A 1 : 2 co-crystal of isonicotinamide and propionic acid

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A 1:2 co-crystal of isonicotinamide and propionic acid

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Key indicators

Single-crystal X-ray study
T = 150 K
Mean σ(C–C) = 0.005 Å
R factor = 0.088
wR factor = 0.198
Data-to-parameter ratio = 17.1

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

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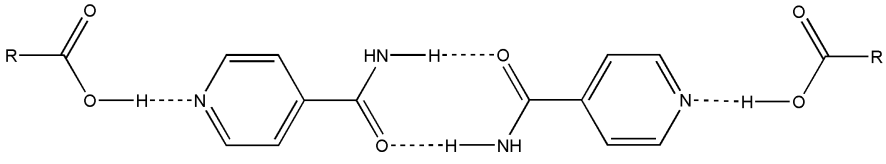
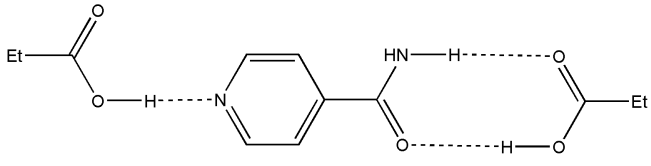
Isonicotinamide has been shown to form many 1:1 co-crystals with monofunctional carboxylic acids, but with propionic acid it forms a co-crystal containing two acid molecules and one isonicotinamide molecule per formula unit, $C_6H_6N_2O\cdot 2C_3H_6O_2$. The crystal structure consists of 'supermolecules' made up of of one isonicotinamide molecule and two acid molecules, and the asymmetric unit contains two of these supermolecules. One of the acid molecules is hydrogen bonded to the pyridine function, and the other to the amide function of the isonicotinamide. Further N—H···O hydrogen bonds connect these supermolecules into chains which run along the [100] direction. The chains are linked into layers perpendicular to (010) by C—H···O and π-stacking interactions. The layers are then linked together by further C—H···O interactions.

Comment

Isonicotinamide has been shown to crystallize with carboxylic acids in a 1:1 stoichiometry to form a robust building block or 'supermolecule' consisting of two amide and two acid molecules, (I) (Aakeröy *et al.*, 2002). When a saturated solution of isonicotinamide in warm propionic acid was allowed to cool, colourless crystalline laths were obtained. Single-crystal X-ray diffraction revealed these to be a co-crystal consisting of isonicotinamide and propionic acid in a 1:2 ratio, *viz*. (II).



(I)



(II)

Similar preparative routes with formic and acetic acids both yielded 1:1 co-crystals (Oswald, 2004). Attempts to prepare a 1:1 co-crystal with propionic acid failed. For example, a 1:1 mixture of propionic acid and isonicotinamide in ethanol yielded only crystals of (II); even in the presence of excess isonicotinamide, the only crystals obtained were isonicotinamide itself and (II).

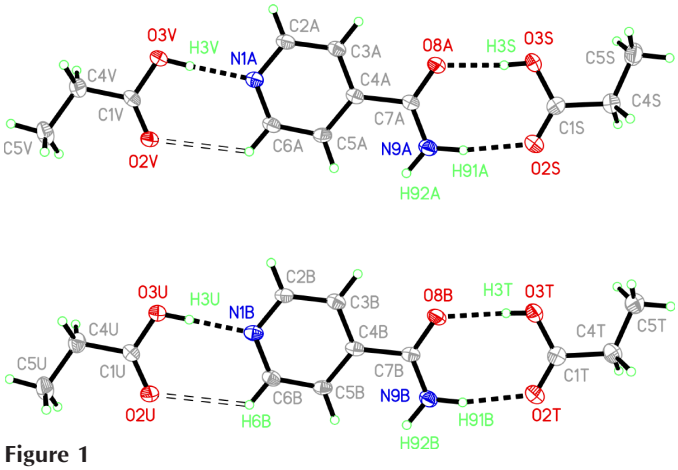


Figure 1
The two crystallographically independent supermolecules, with the atomic numbering. Displacement ellipsoids are drawn at the 30% probability level. Conventional hydrogen bonds are shown in heavy dashes and the H···O distances span 1.78 (4)–1.96 (4) Å (see Table 1). The C—H···O hydrogen bonds (shown as open dashes) are quite weak for this type of interaction (2.73 and 2.72 Å).

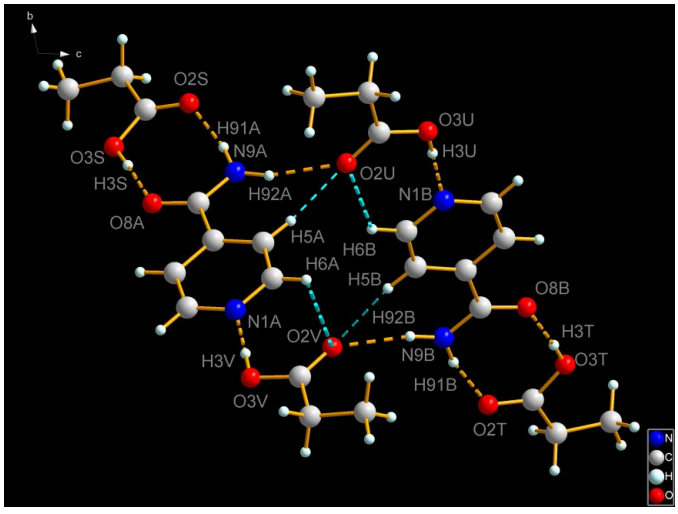


Figure 2
Hydrogen-bonded chains in the crystal structure of (II). Hydrogen bonds link supermolecules into chains. This view is approximately along the direct lattice direction [100]. Hydrogen bonds are shown as dashed lines, weak C—H···O hydrogen bonds are shown in turquoise.

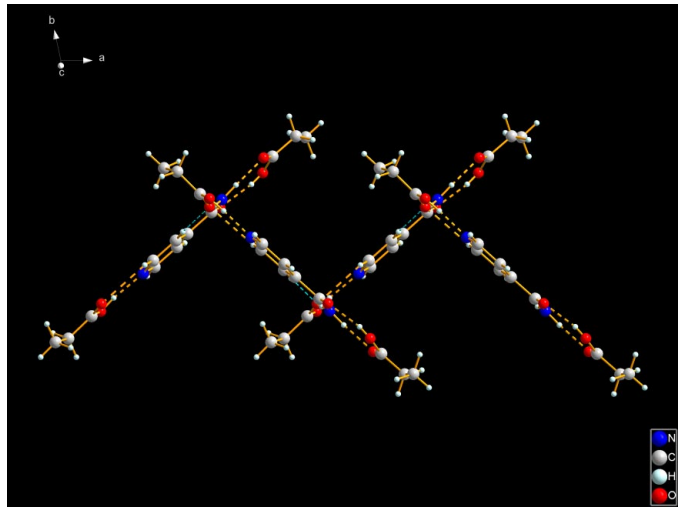


Figure 3
Hydrogen-bonded chains in the crystal structure of (II). Successive supermolecules are approximately perpendicular to each other; this view is perpendicular to (001).

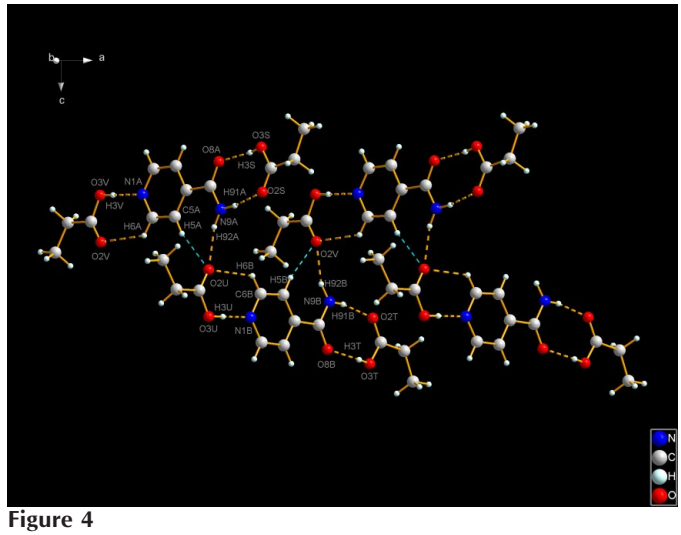


Figure 4
Hydrogen-bonded chains in the crystal structure of (II). View of the chain, showing the atom numbering; view approximately along [010].

The crystal structure of (II) consists of supermolecules comprising two acid and one isonicotinamide molecule. One acid forms an $R_2^2(8)$ motif with the amide moiety (Bernstein *et al.*, 1995). Another acid molecule forms a hydrogen bond to the pyridine N atom, supported by a weaker C—H···O hydrogen bond (Fig. 1 and Table 1). There are two supermolecules in the asymmetric unit and, in the terminology of Aakeröy *et al.* (2002), both are in the *trans–trans* conformation.

The independent supermolecules hydrogen-bond together using the second amide donor and the carbonyl group from the propionic acid molecules located at the pyridine end of the supermolecules. This builds up a helical chain in which successive supermolecules are aligned approximately perpendicular to one another (Figs. 2–4; hydrogen-bond dimensions are listed in Table 1). The chains run along the **a** direction, and they comprise all the conventional N—H···O and O—H···O hydrogen bonds in the crystal structure (see Table 1); additional C—H···O interactions (C5*A*—H5*A*···O2*U* and C5*B*—H5*B*···O2*V*) are also formed within the chains (Desiraju & Steiner, 1999).

Successive helical chains are distributed along the *c* direction at $z = \frac{1}{4}, \frac{3}{4}, \ldots$, *etc.* (Fig. 5). Though there are no direct hydrogen-bonding interactions between neighbouring chains, weak C—H···O interactions are formed between chains located one lattice-repeat away from each other (*e.g.* the red and blue chains in Fig. 5; see also Fig. 6). These interactions involve C2*A*—H2*A*···O3*T* and C2*B*—H2*B*···O3*S*. Supermolecules in neighbouring chains are interleaved to produce stacks of supermolecules along **a** (Fig. 5). Stacks containing only the supermolecules based on isonicotinamide molecule *A* occur at $z = \frac{1}{2}$, while stacks containing only those

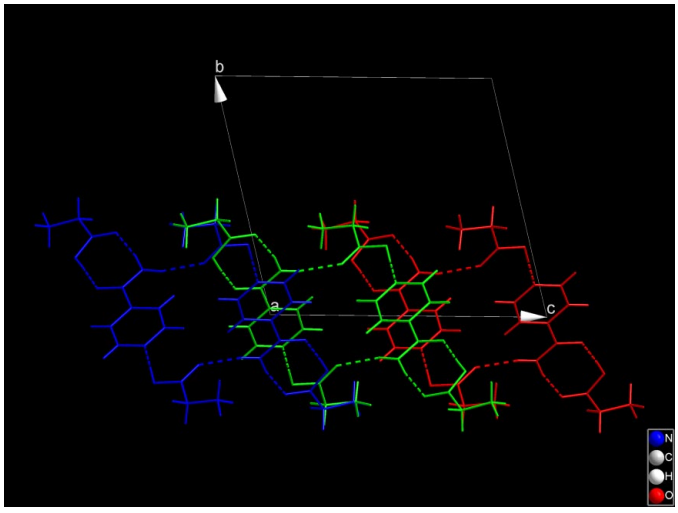


Figure 5
Packing of hydrogen-bonded chains in the crystal structure of (II), forming a layer perpendicular to **b***. Neighbouring chains are distributed along the *c* axis. Different chains (as shown in Figs. 2–4) are shown in different colours. This view is along **a**, *cf.* Fig. 2.

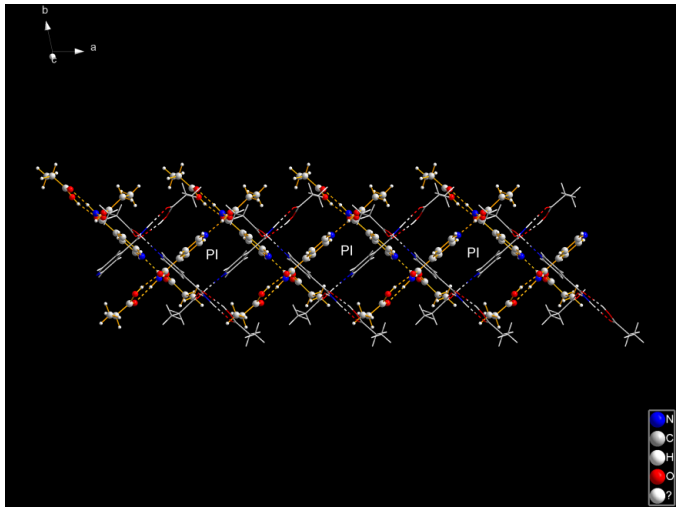


Figure 7
Packing of hydrogen-bonded chains in the crystal structure of (II), forming a layer perpendicular to [010]. Neighbouring chains are connected by π-stacking interactions. This figure shows two chains viewed along [001]. One chain is shown in ball-and-stick representation, the other as wireframe.

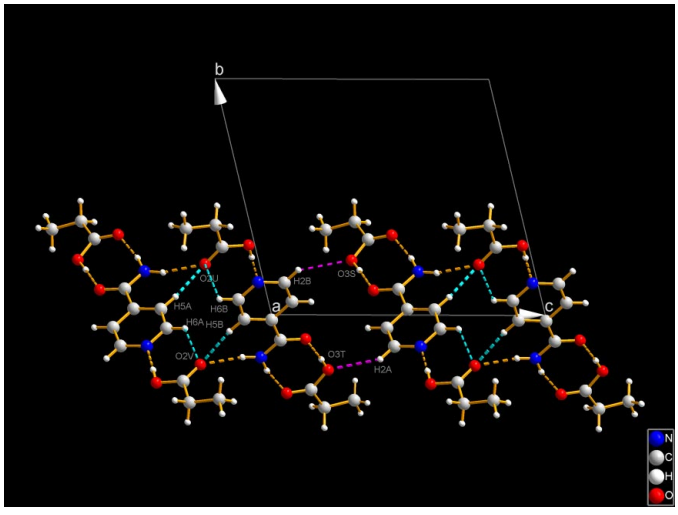


Figure 6
Packing of hydrogen-bonded chains in the crystal structure of (II), forming a layer perpendicular to **b***. As Fig. 5, but with the green molecule deleted to reveal C—H···O hydrogen bonds formed between the blue and red chains shown in Fig. 5. C—H···O hydrogen bonds within chains are shown in turquoise, those between chains are shown in magenta.

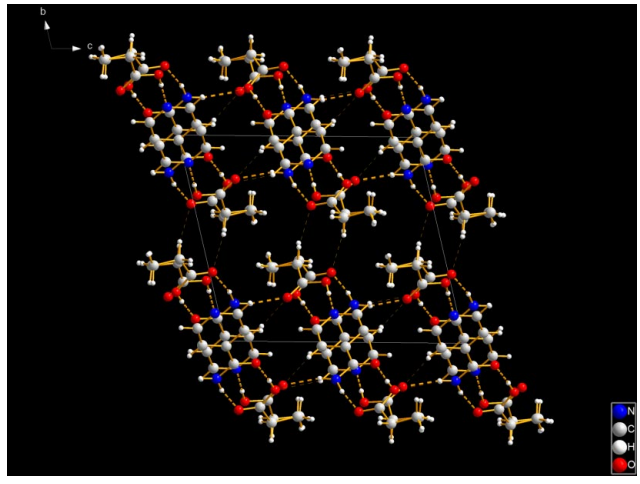


Figure 8
Full packing diagram of the crystal structure of (II), viewed along [100]. Different layers (as shown in Figs. 5–7) are shown in the top and bottom halves of the figure. C—H···O hydrogen bonds connect the layers.

based on molecule *B* occur at z = 0, 1, ... *etc*. Within the stacks, pairs of pyridine moieties are π-stacked across inversion centres (Fig. 7). The stacking distances are 3.34 and 3.33 Å for the *A* and *B* pyridine rings, respectively.

Thus, layers are formed in the *ac*-plane by chains of hydrogen-bonded supermolecules linked by weak C—H···O and π-stacking interactions. The layers are connected *via* C—H···O hydrogen bonds involving pairs of C4*T*—H4*T*1···O2*T* and C4*V*—H4*V*1···O2*S* interactions disposed about inversion centres (Fig. 8).

Experimental

All materials were obtained from Aldrich and used as received. Isonicotinamide (0.50 g, 4.10 mmol) was dissolved in an excess of propionic acid (2.40 g, 32.43 mmol) and warmed until all the solid dissolved. The solution was cooled to room temperature, producing colourless laths.

Crystal data

$C_6H_6N_2O{\cdot}2C_3H_6O_2$
M_r = 270.28
Triclinic, $P\overline{1}$
a = 10.038 (3) Å
b = 11.559 (4) Å
c = 12.740 (4) Å
α = 103.203 (6)°
β = 90.140 (6)°
γ = 102.247 (6)°
V = 1404.5 (8) Å^3
Z = 4
D_x = 1.278 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 1107 reflections
θ = 2.6–22.2°
μ = 0.10 mm^{-1}
T = 150 (2) K
Lath, colourless
0.75 × 0.20 × 0.08 mm

Data collection

Bruker SMART CCD area-detector diffractometer with an Oxford Cryosystems low-temperature device (Cosier & Glazer, 1986)	12519 measured reflections 6498 independent reflections 3362 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{int} = 0.044$
Absorption correction: multi-scan (*SADABS*; Sheldrick, 2004)	$\theta_{max} = 28.9^\circ$ $h = -13 \rightarrow 13$
$T_{min} = 0.783$, $T_{max} = 1.000$	$k = -15 \rightarrow 15$ $l = -17 \rightarrow 17$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0681P)^2 + 0.3798P]$ where $P = (F_o^2 + 2F_c^2)/3$
$R[F^2 > 2\sigma(F^2)] = 0.088$	$(\Delta/\sigma)_{max} < 0.001$
$wR(F^2) = 0.198$	$\Delta\rho_{max} = 0.36$ e Å^{-3}
$S = 1.04$	$\Delta\rho_{min} = -0.21$ e Å^{-3}
6498 reflections	
379 parameters	
H atoms treated by a mixture of independent and constrained refinement	

Table 1
Hydrogen-bonding geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
O3*S*—H3*S*···O8*A*	0.79 (4)	1.86 (4)	2.639 (4)	170 (4)
O3*T*—H3*T*···O8*B*	0.76 (5)	1.89 (5)	2.639 (4)	169 (5)
O3*U*—H3*U*···N1*B*^{i}	0.87 (4)	1.78 (4)	2.649 (4)	177 (5)
O3*V*—H3*V*···N1*A*^{ii}	0.87 (5)	1.79 (5)	2.657 (4)	174 (5)
N9*A*—H91*A*···O2*S*	0.96 (5)	1.92 (4)	2.868 (4)	170 (5)
N9*B*—H91*B*···O2*T*	0.93 (4)	1.96 (4)	2.880 (4)	168 (3)
N9*A*—H92*A*···O2*U*^{iii}	0.92 (3)	2.02 (3)	2.901 (4)	161 (3)
N9*B*—H92*B*···O2*V*	0.93 (3)	2.01 (3)	2.900 (4)	160 (3)
C2*A*—H2*A*···O3*T*^{iv}	0.95	2.50	3.267 (5)	138
C2*B*—H2*B*···O3*S*^{v}	0.95	2.51	3.281 (5)	138
C5*A*—H5*A*···O2*U*^{iii}	0.95	2.40	3.328 (4)	167
C5*B*—H5*B*···O2*V*	0.95	2.39	3.322 (4)	168
C6*A*—H6*A*···O2*V*^{vi}	0.95	2.73	3.348 (4)	123
C6*B*—H6*B*···O2*U*^{i}	0.95	2.72	3.333 (4)	123
C4*T*—H4*T*1···O2*T*^{vii}	0.99	2.58	3.513 (5)	157
C4*V*—H4*V*1···O2*S*^{viii}	0.99	2.57	3.551 (4)	170

Symmetry codes: (i) $1-x, 2-y, -z$; (ii) $1+x, 1+y, z-1$; (iii) $1-x, 1-y, 1-z$; (iv) $x-1, y-1, z$; (v) $x, 1+y, z$; (vi) $x-1, y-1, 1+z$; (vii) $2-x, 1-y, -z$; (viii) $x, y, z-1$.

H atoms were placed on C atoms in calculated positions [U_{iso}(H) = 1.2U_{eq}(C)] and allowed to ride on their parent atoms [C(phenyl)—H = 0.95, C(methylene)—H = 0.99 and C(methyl)—H = 0.98 Å]. Amide and hydroxyl H atoms were located in difference maps and refined freely, the former subject to the restraint N—H = 0.95 (3) Å. The ranges of N—H and O—H bond lengths were 0.91 (2)–0.96 (1) and 0.75 (5)–0.87 (4) Å, respectively.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT* (Bruker, 2003); data reduction: *SAINT* ; program(s) used to solve structure: *SHELXTL* (Sheldrick, 2001); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL, MERCURY* (Taylor & Macrae, 2001) and *DIAMOND* (Crystal Impact, 2004); software used to prepare material for publication: *SHELXTL*, *EnCIFer* (Allen *et al.*, 2004) and *PLATON* (Spek, 2003), as incorporated in *WinGX* (Farrugia, 1999)..

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